

26 20310



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,308

DATE: 03/06/2002 P-5
TIME: 12:44:52

Input Set : A:\1146 PatentIn 3.1.ST25.txt

Output Set: N:\CRF3\03062002\I993308.raw

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3 <110> APPLICANT: Gordon-Kamm, William J.
4     Lowe, Keith S.
5     Larkins, Brian A.
6     Dilkes, Brian R.
7     Sun, Yuejin
9 <120> TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides and Uses Thereof
11 <130> FILE REFERENCE: 1146
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/993,308
14 <141> CURRENT FILING DATE: 2001-11-06
16 <150> PRIOR APPLICATION NUMBER: 60/246,349
17 <151> PRIOR FILING DATE: 2000-11-07
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1372
25 <212> TYPE: DNA
26 <213> ORGANISM: Zea mays
28 <220> FEATURE:
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30 <222> LOCATION: (134)..(904)
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39 ggcgttgctg cag atg ggg aag tac atg cgc aag tgc agg ggc gcc gca      169
40           Met Gly Lys Tyr Met Arg Lys Cys Arg Gly Ala Ala
41           1           5           10
43 ggc gcg gag gtc gcc gcc gtc gag gtt acg cag gtc gtc ggc gtc cgg      217
44 Gly Ala Glu Val Ala Ala Val Glu Val Thr Gln Val Val Gly Val Arg
45           15           20           25
47 acg agg tcc agg tcc gcg gcg gcg acc ggc ggt gtc gcg aag gtc gcc      265
48 Thr Arg Ser Arg Ser Ala Ala Ala Thr Gly Gly Val Ala Lys Val Ala
49           30           35           40
51 ccg agg agg aag agg gcg ccg gcg ggg gag cct gct gcc gcc gtg agc      313
52 Pro Arg Arg Lys Arg Ala Pro Ala Gly Glu Pro Ala Ala Ala Val Ser
53 45           50           55           60
55 gct ggt ggg gac ggc gga agc tgc tac atc cac ctg cgt agc cgc atg      361
56 Ala Gly Gly Asp Gly Gly Ser Cys Tyr Ile His Leu Arg Ser Arg Met
57           65           70           75
59 ctg ttc atg gca ccg cct cag ccg cag ccg tcg gtt gac tcg gtt ccg      409
60 Leu Phe Met Ala Pro Pro Gln Pro Gln Pro Ser Val Asp Ser Val Pro
61           80           85           90
63 acc ccg gtg gag gct gct gat ggc gct gca gga cag cag ggc gcg gcg      457

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64 Thr Pro Val Glu Ala Ala Asp Gly Ala Ala Gly Gln Gln Gly Ala Ala
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67 ctc gcg gcc ggg ctc tcg cgt tgc tcc agc acg gcg tcg tcg gtg aac      505
68 Leu Ala Ala Gly Leu Ser Arg Cys Ser Ser Thr Ala Ser Ser Val Asn
69      110          115          120
71 ttg ggc ttg ggg ggt cag cgc ggg agc cac acc tgc cgc tcc tac gac      553
72 Leu Gly Leu Gly Gly Gln Arg Gly Ser His Thr Cys Arg Ser Tyr Asp
73 125          130          135          140
75 gct gca gag gct ggc ggg gat cac gtc ctg gtg gat gtc tcg gcg gcg      601
76 Ala Ala Glu Ala Gly Gly Asp His Val Leu Val Asp Val Ser Ala Ala
77          145          150          155
79 agc aac tcc ggg agc ggc cca gac cgc gag agg cga gag acg acg cca      649
80 Ser Asn Ser Gly Ser Gly Pro Asp Arg Glu Arg Arg Glu Thr Thr Pro
81          160          165          170
83 tcg agc cgg gcg cac ggc gag ctc agc gat ctg gag tcg gat ctg gcg      697
84 Ser Ser Arg Ala His Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu Ala
85          175          180          185
87 ggg cac aag act ggc ccg tcg cta ccg gcg gca acg ccg gct gcg gag      745
88 Gly His Lys Thr Gly Pro Ser Leu Pro Ala Ala Thr Pro Ala Ala Glu
89          190          195          200
91 ctg atc gtg ccg cca gca cac gag atc cag gag ttc ttc gcc gcc gcc      793
92 Leu Ile Val Pro Pro Ala His Glu Ile Gln Glu Phe Phe Ala Ala Ala
93 205          210          215          220
95 gag gcg gcc cag gcc aag cgc ttt gct tcc aag tac aac ttc gac ttc      841
96 Glu Ala Ala Gln Ala Lys Arg Phe Ala Ser Lys Tyr Asn Phe Asp Phe
97          225          230          235
99 gtc cgc ggc gtg ccc ctc gac gcc ggc ggc cgg ttc gag tgg gcg ccg      889
100 Val Arg Gly Val Pro Leu Asp Ala Gly Gly Arg Phe Glu Trp Ala Pro
101          240          245          250
103 gtg gtc agc atc tga agcgagcgtg cgtccggtgc aaggtgaagc tagaaagaga      944
104 Val Val Ser Ile
105          255
107 aaagatgccc cccccccccc cccccaacaa acataacgga gaagagaaaa accaaacaat      1004
109 taagcagctt tatatagcct aagctaacca ccaccattca tctcgtccaa atgcatgcct      1064
111 tgctttttctc tggagctagc aggagcgtag ttattattta gtactacttt acttattcag      1124
113 aggttatctt gaccccgata gatcaatccg cttactgtgt aatttctctc atgcatctct      1184
115 tagatggagt ttaatcgtct taatttatta ctgtacagca gcttgsttgg cttgcaaaga      1244
117 aagatctggt ttgtctcaaa aaaaaaaaaa aaaaaaaaaa aaaaagggcg gccgctctag      1304
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125 <211> LENGTH: 256
126 <212> TYPE: PRT
127 <213> ORGANISM: Zea mays
129 <400> SEQUENCE: 2
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132 1          5          10          15
135 Ala Ala Val Glu Val Thr Gln Val Val Gly Val Arg Thr Arg Ser Arg
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140      35      40      45
143 Arg Ala Pro Ala Gly Glu Pro Ala Ala Ala Val Ser Ala Gly Gly Asp
144      50      55      60
147 Gly Gly Ser Cys Tyr Ile His Leu Arg Ser Arg Met Leu Phe Met Ala
148 65      70      75      80
151 Pro Pro Gln Pro Gln Pro Ser Val Asp Ser Val Pro Thr Pro Val Glu
152      85      90      95
155 Ala Ala Asp Gly Ala Ala Gly Gln Gln Gly Ala Ala Leu Ala Ala Gly
156      100     105     110
159 Leu Ser Arg Cys Ser Ser Thr Ala Ser Ser Val Asn Leu Gly Leu Gly
160      115     120     125
163 Gly Gln Arg Gly Ser His Thr Cys Arg Ser Tyr Asp Ala Ala Glu Ala
164      130     135     140
167 Gly Gly Asp His Val Leu Val Asp Val Ser Ala Ala Ser Asn Ser Gly
168 145     150     155     160
171 Ser Gly Pro Asp Arg Glu Arg Arg Glu Thr Thr Pro Ser Ser Arg Ala
172      165     170     175
175 His Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu Ala Gly His Lys Thr
176      180     185     190
179 Gly Pro Ser Leu Pro Ala Ala Thr Pro Ala Ala Glu Leu Ile Val Pro
180      195     200     205
183 Pro Ala His Glu Ile Gln Glu Phe Phe Ala Ala Ala Glu Ala Ala Gln
184      210     215     220
187 Ala Lys Arg Phe Ala Ser Lys Tyr Asn Phe Asp Phe Val Arg Gly Val
188 225     230     235     240
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192      245     250     255
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196 <211> LENGTH: 1089
197 <212> TYPE: DNA
198 <213> ORGANISM: Zea mays
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (154)..(726)
203 <223> OTHER INFORMATION:
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209 tctcctggcc tctgccgccc cgtgcacag aatcgcttgg tgcaccctgc gagggcctcc      120
211 tcgaaaccct agcttgccca gcccctccgg gcc atg ggc aag tac atg cgc aag      174
212      Met Gly Lys Tyr Met Arg Lys
213      1      5
215 gcc aag gct tcc agc gag gtt gtc atc atg gat gtc gcc gcc gct ccg      222
216 Ala Lys Ala Ser Ser Glu Val Val Ile Met Asp Val Ala Ala Ala Pro
217      10      15      20
219 ctc gga gtc cgc acc cga gcg cgc gcc ctc gcg ctg cag cgt ctg cag      270
220 Leu Gly Val Arg Thr Arg Ala Arg Ala Leu Ala Leu Gln Arg Leu Gln
221      25      30      35
223 gag cag cag acg cag tgg gag gaa ggt gct ggc ggc gag tac ctg gag      318

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228 Leu Arg Asn Arg Arg Leu Glu Lys Leu Pro Pro Pro Pro Ala Thr Thr
229                      60                      65                      70
231 agg agg tcg ggc ggg agg aaa gcg gca gcc gag gcc gcc gca act aag      414
232 Arg Arg Ser Gly Gly Arg Lys Ala Ala Ala Glu Ala Ala Ala Thr Lys
233                      75                      80                      85
235 gag gct gag gcg tcg tac ggg gag aac atg ctc gag ttg gag gcc atg      462
236 Glu Ala Glu Ala Ser Tyr Gly Glu Asn Met Leu Glu Leu Glu Ala Met
237                      90                      95                      100
239 gag agg att acc agg gag acg acg cct tgc agc ttg att aac acc cag      510
240 Glu Arg Ile Thr Arg Glu Thr Thr Pro Cys Ser Leu Ile Asn Thr Gln
241                      105                      110                      115
243 atg act agc act cct ggg tcc acg aga tcc agc cac tct tgc cac cgc      558
244 Met Thr Ser Thr Pro Gly Ser Thr Arg Ser Ser His Ser Cys His Arg
245 120                      125                      130                      135
247 agg gtg aac gct cct ccg gtg cac gcc gtc cca agt tcg agg gag atg      606
248 Arg Val Asn Ala Pro Val His Ala Val Pro Ser Ser Arg Glu Met
249                      140                      145                      150
251 aat gag tac ttc gct gcc gaa cag cga cgc caa caa cag gat ttc att      654
252 Asn Glu Tyr Phe Ala Ala Glu Gln Arg Arg Gln Gln Gln Asp Phe Ile
253                      155                      160                      165
255 gac aag tac aac ttc gat cct gca aac gac tgc cct ctc cca ggc agg      702
256 Asp Lys Tyr Asn Phe Asp Pro Ala Asn Asp Cys Pro Leu Pro Gly Arg
257                      170                      175                      180
259 ttt gag tgg gtg aag cta gac tga tggattcaga gggacgagag agcagcaggc      756
260 Phe Glu Trp Val Lys Leu Asp
261                      185                      190
263 atggaatgga atggaactca cccccgcgtc cctccacacc accccagcgt tgtggcagag      816
265 ggcataaccg tcgtgttagc ttctgtttctg ctgtaaaaaa aaacttagtg ttttagcatg      876
267 tagccttaat tggctgtgtg ttacagtaca gaactgatgc tgagttacaa caccctgatc      936
269 tggctcttgat ctgateccctc aactccaatg taacccttaa cagctcattc tgtaaggaaac      996
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277 <211> LENGTH: 190
278 <212> TYPE: PRT
279 <213> ORGANISM: Zea mays
281 <400> SEQUENCE: 4
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287 Met Asp Val Ala Ala Ala Pro Leu Gly Val Arg Thr Arg Ala Arg Ala
288                      20                      25                      30
291 Leu Ala Leu Gln Arg Leu Gln Glu Gln Gln Thr Gln Trp Glu Glu Gly
292                      35                      40                      45
295 Ala Gly Gly Glu Tyr Leu Glu Leu Arg Asn Arg Arg Leu Glu Lys Leu
296                      50                      55                      60
299 Pro Pro Pro Pro Ala Thr Thr Arg Arg Ser Gly Gly Arg Lys Ala Ala

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300 65              70              75              80
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304              85              90              95
307 Met Leu Glu Leu Glu Ala Met Glu Arg Ile Thr Arg Glu Thr Thr Pro
308              100             105             110
311 Cys Ser Leu Ile Asn Thr Gln Met Thr Ser Thr Pro Gly Ser Thr Arg
312              115             120             125
315 Ser Ser His Ser Cys His Arg Arg Val Asn Ala Pro Pro Val His Ala
316              130             135             140
319 Val Pro Ser Ser Arg Glu Met Asn Glu Tyr Phe Ala Ala Glu Gln Arg
320 145             150             155             160
323 Arg Gln Gln Gln Asp Phe Ile Asp Lys Tyr Asn Phe Asp Pro Ala Asn
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328              180             185             190
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332 <211> LENGTH: 841
333 <212> TYPE: DNA
334 <213> ORGANISM: Zea mays
336 <220> FEATURE:
337 <221> NAME/KEY: CDS
338 <222> LOCATION: (159)..(839)
339 <223> OTHER INFORMATION: The 'r' at location 491 stands for g or a.
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347 agcgagaaga aggcagtgtc gcggcggcgt tccgtaag atg ggg aag tac atg cgc      176
348                               Met Gly Lys Tyr Met Arg
349                               1              5
351 aag cgc agg ggg gcc gcg ggc gag ggg gtg gcc gca gtc gag gtc tcg      224
352 Lys Arg Arg Gly Ala Ala Gly Glu Gly Val Ala Ala Val Glu Val Ser
353              10              15              20
355 cag gtc gtc ggc gtc cgg acg agg tcc agg tcc gcg gcg gcg acc ggc      272
356 Gln Val Val Gly Val Arg Thr Arg Ser Arg Ser Ala Ala Ala Thr Gly
357              25              30              35
359 ggc ggt gtc gcg aag gtc gct ccg ccg agg agg aag aag gcg ctg ctg      320
360 Gly Gly Val Ala Lys Val Ala Pro Pro Arg Arg Lys Lys Ala Leu Leu
361              40              45              50
363 ccc gcc gcg aac gtg acg acg tcg ggg gag cct ggt gcc gtg ggc gct      368
364 Pro Ala Ala Asn Val Thr Thr Ser Gly Glu Pro Gly Ala Val Gly Ala
365 55              60              65              70
367 ggt ggt ggg gac ggc gga agc tgc tgc tac atc cac ctg cgg agc cgc      416
368 Gly Gly Gly Asp Gly Gly Ser Cys Cys Tyr Ile His Leu Arg Ser Arg
369              75              80              85
371 atg ctg ttc atg gca gca cct cag cag caa ccg tcg gcg gct ctg acg      464
372 Met Leu Phe Met Ala Ala Pro Gln Gln Gln Pro Ser Ala Ala Leu Thr
373              90              95              100
375 ccg gtg gag gct gct ggt gcg gca car caa ggc ggg gtg gtg gcg ctc      512
W--> 376 Pro Val Glu Ala Ala Gly Ala Ala Xaa Gln Gly Gly Val Val Ala Leu

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6